

DAYER
SEQUENCE LISTING

<110> Dayer, Jean-Michel
Burger, Danielle
Kohno, Tadahiko
Edwards III, Carl K.

<120> APO-A-1 REGULATION OF T-CELL SIGNALING

<130> 06843.0035-00000

<140> Not Yet Assigned

<141> 2001-03-13

<150> 60/189,008

<151> 2000-03-13

<150> 60/193,551

<151> 2000-03-31

<160> 4

<170> PatentIn Ver. 2.1

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<211> 801

<212> DNA

<213> Homo sapiens

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<221> sig_peptide

<222> (20)..(91)

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cagaagggtg	agccgctgcg	cgcagagctc	caagagggcg	cgcgccagaa	gctgcacgag	499
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gacgcgctgc	gcacgcattc	ggccccctac	agcgacgagc	tgcgccagcg	cttggccgcg	619
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<211> 267

<212> PRT

<213> Homo sapiens

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			20					25					30		

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Asp Arg Val₃₅ Lys Asp Leu Ala Thr Val Tyr Val₄₀ Asp Val₄₅ Leu Lys Asp
 Ser Gly Arg Asp Tyr Val₅₀ Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys₅₅
 Gln Leu Asn Leu Lys Leu₆₅ Leu Asp Asn Trp₇₀ Asp₇₅ Ser Val Thr Ser Thr₈₀
 Phe Ser Lys Leu Arg₈₅ Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp₉₀
 Asp Asn Leu Glu₁₀₀ Lys Glu Thr Glu Gly₁₀₅ Leu Arg Gln Glu Met Ser Lys₁₁₀
 Asp Leu Glu Glu Val₁₁₅ Lys Ala Lys Val₁₂₀ Gln Pro Tyr Leu Asp Asp Phe₁₂₅
 Gln Lys Lys Trp Gln Glu Glu₁₃₀ Met Glu Leu Tyr Arg Gln Lys Val Glu₁₃₅
 Pro Leu Arg Ala Glu₁₄₀ Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu₁₄₅
 Leu Gln Glu Lys₁₅₀ Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala₁₅₅
 Arg Ala His Val₁₆₀ Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp₁₆₅
 Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn₁₇₀
 Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu₁₇₅
 Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln₁₈₀
 Gly Leu Leu Pro Val₁₈₅ Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala₁₉₀
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Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu
 50 55 60

Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu
 65 70 75 80

Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys
 85 90 95

Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met
 100 105 110

Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu
 115 120 125

Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu
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Thr His Leu Ala Pro Tyr Ser Asp Glu Leu
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ggcctgaggc	aggagatgag	caaggatctg	gaggagggtga	aggccaaggt	gcagccctac	391
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acgcatctgg	ccccctacag	cgacgagctg				601